#2   OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/802,741

DATE: 04/26/2001
TIME: 10:40:02

Input Set : N:\Crf3\RULE60\09802741.txt
Output Set: N:\CRF3\04262001\I802741.raw

ENTERED

SEQUENCE LISTING

```
C-->  3 (1) GENERAL INFORMATION:
      5      (i) APPLICANT: Fisher, Douglas A.
      6                     Gooding, Doug
      7                     Streeter, Dave
C-->  9     (ii) TITLE OF INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
     11    (iii) NUMBER OF SEQUENCES: 14
     13     (iv) CORRESPONDENCE ADDRESS:
     14          (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
     15          (B) STREET: 3174 Porter Dr.
     16          (C) CITY: Palo Alto
     17          (D) STATE: CA
     18          (E) COUNTRY: USA
     19          (F) ZIP: 94304
     21      (v) COMPUTER READABLE FORM:
     22          (A) MEDIUM TYPE: Diskette
     23          (B) COMPUTER: IBM Compatible
     24          (C) OPERATING SYSTEM: DOS
     25          (D) SOFTWARE: FastSEQ for Windows Version 2.0
     27     (vi) CURRENT APPLICATION DATA:
C--> 28          (A) APPLICATION NUMBER: US/09/802,741
C--> 29          (B) FILING DATE: 08-Mar-2001
     30          (C) CLASSIFICATION:
     32    (vii) PRIOR APPLICATION DATA:
     33          (A) APPLICATION NUMBER: 09/240,359
     34          (B) FILING DATE:
     37   (viii) ATTORNEY/AGENT INFORMATION:
     38          (A) NAME: Billings, Lucy J.
     39          (B) REGISTRATION NUMBER: 36,749
     40          (C) REFERENCE/DOCKET NUMBER: PF-0442 US
     42     (ix) TELECOMMUNICATION INFORMATION:
     43          (A) TELEPHONE: 650-855-0555
     44          (B) TELEFAX: 650-845-4166
     47 (2) INFORMATION FOR SEQ ID NO: 1:
     49      (i) SEQUENCE CHARACTERISTICS:
     50          (A) LENGTH: 593 amino acids
     51          (B) TYPE: amino acid
     52          (C) STRANDEDNESS: single
     53          (D) TOPOLOGY: linear
     55    (vii) IMMEDIATE SOURCE:
     56          (A) LIBRARY: PROSNOT06
     57          (B) CLONE: 828228
     59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     62 Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
     63  1               5                  10                  15
     64 Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser
     65               20                  25                  30
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66   Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn
67           35                  40                  45
68   Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp
69           50                  55                  60
70   Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro
71   65                  70                  75                  80
72   Val Ala Ile Lys Gln Leu Ser Ala Gly Val Glu Asp Lys Arg Thr Thr
73                   85                  90                  95
74   Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg Arg Val Val
75               100                 105                 110
76   Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser Gly Gln Val
77           115                 120                 125
78   Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu Gly Gln Arg
79           130                 135                 140
80   Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val
81   145                 150                 155                 160
82   Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu
83               165                 170                 175
84   Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly
85               180                 185                 190
86   Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met
87           195                 200                 205
88   Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys
89           210                 215                 220
90   Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val
91   225                 230                 235                 240
92   Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu
93               245                 250                 255
94   Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu
95               260                 265                 270
96   Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe
97           275                 280                 285
98   Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp
99           290                 295                 300
100  Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val
101  305                 310                 315                 320
102  Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys
103                      325                 330                 335
104  Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His
105               340                 345                 350
106  Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg
107           355                 360                 365
108  Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His
109           370                 375                 380
110  His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile
111  385                 390                 395                 400
112  Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met
113                      405                 410                 415
114  Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met
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PATENT APPLICATION: US/09/802,741   TIME: 10:40:02

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115              420              425              430
116   Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu
117          435              440              445
118   His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser
119      450              455              460
120   Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu
121   465              470              475              480
123   Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu
124              485              490              495
125   Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala
126              500              505              510
127   Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val
128      515              520              525
129   Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp
130      530              535              540
131   Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met
132   545              550              555              560
133   Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu
134              565              570              575
135   Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys
136              580              585              590
137   Ala
140   (2) INFORMATION FOR SEQ ID NO: 2:
142         (i) SEQUENCE CHARACTERISTICS:
143             (A) LENGTH: 1997 base pairs
144             (B) TYPE: nucleic acid
145             (C) STRANDEDNESS: single
146             (D) TOPOLOGY: linear
148        (vii) IMMEDIATE SOURCE:
149             (A) LIBRARY: PROSNOT06
150             (B) CLONE: 828228
152         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
154   GCTCCCCGCG GCGGCTGGCG TCGGGAAAGT ACAGTAAAAA GTCCGAGTGC AGCCGCCGGG      60
155   CGCAGGATGG GATCCGGCTC CTCCAGCTAC CGGCCCAAGG CCATCTACCT GGACATCGAT     120
156   GGACGCATTC AGAAGGTAAT CTTCAGCAAG TACTGCAACT CCAGCGACAT CATGGACCTG     180
157   TTCTGCATCG CCACCGGCCT GCCTCGGAAC ACGACCATCT CCCTGCTGAC CACCGACGAC     240
158   GCCATGGTCT CCATCGACCC CACCATGCCC GCGAATTCAG AACGCACTCC GTACAAAGTG     300
159   AGACCTGTGG CCATCAAGCA ACTCTCCGCT GGTGTCGAGG ACAAGAGAAC CACAAGCCGT     360
160   GGCCAGTCTG CTGAGAGACC ACTGAGGGAC AGACGGGTTG TGGGCCTGGA GCAGCCCCGG     420
161   AGGGAAGGAG CATTTGAAAG TGGACAGGTA GAGCCCAGGC CCAGAGAGCC CCAGGGCTGC     480
162   TACCAGGAAG GCCAGCGCAT CCCTCCAGAG AGAGAAGAAT TAATCCAGAG CGTGCTGGCG     540
163   CAGGTTGCAG AGCAGTTCTC AAGAGCATTC AAAATCAATG AACTGAAAGC TGAAGTTGCA     600
164   AATCACTTGG CTGTCCTAGA GAAACGCGTG GAATTGGAAG GACTAAAAGT GGTGGAGATT     660
165   GAGAAATGCA AGAGTGACAT TAAGAAGATG AGGGAGGAGC TGGCGGCCAG AAGCAGCAGG     720
166   ACCAACTGCC CCTGTAAGTA CAGTTTTTTG GATAACCACA AGAAGTTGAC TCCTCGACGC     780
167   GATGTTCCCA CTTACCCCAA GTACCTGCTC TCTCCAGAGA CCATCGAGGC CCTGCGGGAAG    840
168   CCGACCTTTG ACGTCTGGCT TTGGGAGCCC AATGAGATGC TGAGCTGCCT GGAGCACATG     900
169   TACCACGACC TCGGGCTGGT CAGGGACTTC AGCATCAACC CTGTCACCCT CAGGAGGTGG     960
170   CTGTTCTGTG TCCACGACAA CTACAGAAAC AACCCCTTCC ACAACTTCCG GCACTGCTTC    1020
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171  TGCGTGGCCC AGATGATGTA CAGCATGGTC TGGCTCTGCA GTCTCCAGGA GAAGTTCTCA  1080
172  CAAACGGATA TCCTGATCCT AATGACAGCG GCCATCTGCC ACGATCTGGA CCATCCCGGC  1140
173  TACAACAACA CGTACCAGAT CAATGCCCGC ACAGAGCTGG CGGTCCGCTA CAATGACATC  1200
174  TCACCGCTGG AGAACCACCA CTGCGCCGTG GCCTTCCAGA TCCTCGCCGA GCCTGAGTGC  1260
175  AACATCTTCT CCAACATCCC ACCTGATGGG TTCAAGCAGA TCCGACAGGG AATGATCACA  1320
176  TTAATCTTGG CCACTGACAT GGCAAGACAT GCAGAAATTA TGGATTCTTT CAAAGAGAAA  1380
177  ATGGAGAATT TTGACTACAG CAACGAGGAG CACATGACCC TGCTGAAGAT GATTTTGATA  1440
178  AAATGCTGTG ATATCTCTAA CGAGGTCCGT CCAATGGAAG TCGCAGAGCC TTGGGTGGAC  1500
179  TGTTTATTAG AGGAATATTT TATGCAGAGC GACCGTGAGA AGTCAGAAGG CCTTCCTGTG  1560
180  GCACCGTTCA TGGACCGAGA CAAAGTGACC AAGGCCACAG CCCAGATTGG GTTCATCAAG  1620
181  TTTGTCCTGA TCCCAATGTT TGAAACAGTG ACCAAGCTCT TCCCCATGGT TGAGGAGATC  1680
182  ATGCTGCAGC CACTTTGGGA ATCCCGAGAT CGCTACGAGG AGCTGAAGCG GATAGATGAC  1740
183  GCCATGAAAG AGTTACAGAA GAAGACTGAC AGCTTGACGT CTGGGGCCAC CGAGAAGTCC  1800
184  AGAGAGAGAA GCAGAGATGT GAAAAACAGT GAAGGAGACT GTGCCTGAGG AAAGCGGGGG  1860
185  GCGTGGCTGC AGTTCTGGAC GGGCTGGCCG AGCTGCGCGG GATCCTTGTG CAGGGAAGAG  1920
186  CTGCCCTGGG CACCTGGCAC CACAAGACCA TGTTTTCTAA GAACCATTTT GTTCACTGAT  1980
187  ACAAAAAAAA AAAAAAA                                                  1997
189  (2) INFORMATION FOR SEQ ID NO: 3:
191       (i) SEQUENCE CHARACTERISTICS:
192           (A) LENGTH: 713 amino acids
193           (B) TYPE: amino acid
194           (C) STRANDEDNESS: single
195           (D) TOPOLOGY: linear
197      (vii) IMMEDIATE SOURCE:
198           (A) LIBRARY: THP1PLB02
199           (B) CLONE: 156196
201       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
203  Leu Ala Cys Phe Leu Asp Lys His His Asp Ile Ile Ile Ile Asp His
204   1               5                  10                  15
205  Arg Asn Pro Arg Gln Leu Asp Ala Glu Ala Leu Cys Arg Ser Ile Arg
206              20                  25                  30
207  Ser Ser Lys Leu Ser Glu Asn Thr Val Ile Val Gly Val Val Arg Arg
208              35                  40                  45
209  Val Asp Arg Glu Glu Leu Ser Val Met Pro Phe Ile Ser Ala Gly Phe
210       50                  55                  60
211  Thr Arg Arg Tyr Val Glu Asn Pro Asn Ile Met Ala Cys Tyr Asn Glu
212  65                  70                  75                  80
213  Leu Leu Gln Leu Glu Phe Gly Glu Val Arg Ser Gln Leu Lys Leu Arg
214              85                  90                  95
215  Ala Cys Asn Ser Val Phe Thr Ala Leu Glu Asn Ser Glu Asp Ala Ile
216              100                 105                 110
217  Glu Ile Thr Ser Glu Asp Arg Phe Ile Gln Tyr Ala Asn Pro Ala Phe
218              115                 120                 125
219  Glu Thr Thr Met Gly Tyr Gln Ser Gly Glu Leu Ile Gly Lys Glu Leu
220       130                 135                 140
221  Gly Glu Val Pro Ile Asn Glu Lys Lys Ala Asp Leu Leu Asp Thr Ile
222  145                 150                 155                 160
223  Asn Ser Cys Ile Arg Ile Gly Lys Glu Trp Gln Gly Ile Tyr Tyr Ala
224              165                 170                 175
```

```
225  Lys Lys Lys Asn Gly Asp Asn Ile Gln Gln Asn Val Lys Ile Ile Pro
226              180                 185                 190
227  Val Ile Gly Gln Gly Gly Lys Ile Arg His Tyr Val Ser Ile Ile Arg
228              195                 200                 205
229  Val Cys Asn Gly Asn Asn Lys Ala Glu Lys Ile Ser Glu Cys Val Gln
230          210                 215                 220
231  Ser Asp Thr Arg Thr Asp Asn Gln Thr Gly Lys His Lys Asp Arg Arg
232  225                 230                 235                 240
233  Lys Gly Ser Leu Asp Val Lys Ala Val Ala Ser Arg Ala Thr Glu Val
234              245                 250                 255
235  Ser Ser Gln Arg Arg His Ser Ser Met Ala Arg Ile His Ser Met Thr
236              260                 265                 270
237  Ile Glu Ala Pro Ile Thr Lys Val Ile Asn Val Ile Asn Ala Ala Gln
238          275                 280                 285
239  Glu Ser Ser Pro Met Pro Val Thr Glu Ala Leu Asp Arg Val Leu Glu
240          290                 295                 300
241  Ile Leu Arg Thr Thr Glu Leu Tyr Ser Pro Gln Phe Gly Ala Lys Asp
242  305                 310                 315                 320
243  Asp Asp Pro His Ala Asn Asp Leu Val Gly Gly Leu Met Ser Asp Gly
244              325                 330                 335
245  Leu Arg Arg Leu Ser Gly Asn Glu Tyr Val Leu Ser Thr Lys Asn Thr
246              340                 345                 350
247  Gln Met Val Ser Ser Asn Ile Ile Thr Pro Ile Ser Leu Asp Asp Val
248          355                 360                 365
249  Pro Pro Arg Ile Ala Arg Ala Met Glu Asn Glu Glu Tyr Trp Asp Phe
250          370                 375                 380
251  Asp Ile Phe Glu Leu Glu Ala Ala Thr His Asn Arg Pro Leu Ile Tyr
252  385                 390                 395                 400
253  Leu Gly Leu Lys Met Phe Ala Arg Phe Gly Ile Cys Glu Phe Leu His
254              405                 410                 415
255  Cys Ser Glu Ser Thr Leu Arg Ser Trp Leu Gln Ile Ile Glu Ala Asn
256              420                 425                 430
257  Tyr His Ser Ser Asn Pro Tyr His Asn Ser Thr His Ser Ala Asp Val
258          435                 440                 445
259  Leu His Ala Thr Ala Tyr Phe Leu Ser Lys Glu Arg Ile Lys Glu Thr
260          450                 455                 460
261  Leu Asp Pro Ile Asp Glu Val Ala Ala Leu Ile Ala Ala Thr Ile His
262  465                 470                 475                 480
263  Asp Val Asp His Pro Gly Arg Thr Asn Ser Phe Leu Cys Asn Ala Gly
264              485                 490                 495
265  Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His
266          500                 505                 510
267  His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn
268          515                 520                 525
269  Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly
270          530                 535                 540
271  Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His
272  545                 550                 555                 560
273  Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu
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VERIFICATION SUMMARY   DATE: 04/26/2001
PATENT APPLICATION: US/09/802,741   TIME: 10:40:03

Input Set : **N:\Crf3\RULE60\09802741.txt**
Output Set: **N:\CRF3\04262001\I802741.raw**

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]